09-830-972

```
OM protein - nucleic search, using frame_plus_p2n model

                    Copyright (c) 1993 - 2005 Compugen Ltd.
                         GenCore version 5.1.6

Run on:        June 22, 2005, 09:17:28 ; Search time 0.001 Seconds
                                         (without alignments)
                                         1481.544 Million cell updates/sec

Title:         US-09-830-972-29-FUSED
Perfect score: 1850
Sequence:      1 MEDLDQSPLVSSDSPPRQ.........VKDAMAKIQAKIPGLKRKAE 361

Scoring table: BLOSUM62
               Xgapop  10.0 , Xgapext    0.1
               Ygapop  10.0 , Ygapext    0.5
               Fgapop   6.0 , Fgapext    7.0
               Delop    6.0 , Delext     7.0

Searched:      1 seqs, 2052 residues

Total number of hits satisfying chosen parameters:      2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model  -DEV=soft  -Q=fused.pep  -DB=ab015639.seq  -SUFFIX=pto
-OUT=ge.res  -MINMATCH=0.1  -LOOPCL=0  -LOOPEXT=0  -UNITS=bits  -START=1  -END=-1
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-THR_MAX=100  -THR_MIN=0  -ALIGN=15  -MODB=LOCAL  -OUTFMT=pto  -NORM=ext
-HEAPSIZE=500  -MINLEN=0  -MAXLEN=2000000000  -NCPU=6  -NO_XLPXY  -NEG_SCORES=0
-LONGLOG  -THREADS=1  -XGAPOP=10  -XGAPEXT=0.1  -FGAPOP=6  -FGAPEXT=7  -YGAPOP=10
-YGAPEXT=0.5  -DELOP=6  -DELEXT=7

Database :      ab015639.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES

Result        Query
No.   Score   Match Length DB   ID                  Description
----  ------  ----- ------ --   ----------          -----------
  1  1825.8   98.7   2052  1    ab015639                           TOIG of: ab01563
c 2   111.7    6.0   2052  1    ab015639                           TOIG of: ab01563

                             ALIGNMENTS

RESULT 1
ab015639
; TOIG of: ab015639  check: 3818  from: 1  to: 2052

; LOCUS       AB015639              2052 bp    mRNA       linear      PRI 03-SEP-1999
; DEFINITION  Homo sapiens ASY mRNA, complete cds.
; ACCESSION   AB015639
; VERSION     AB015639.1  GI:5821139
; KEYWORDS    ASY.
; SOURCE      Homo sapiens (human)
;  ORGANISM   Homo sapiens
;            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1  (bases 1 to 2052)
;  AUTHORS    Yutsudo,M.
```

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;  TITLE      Isolation of a cell death-inducing gene
;  JOURNAL    Published Only in DataBase (1999)
;  REFERENCE  2  (bases 1 to 2052)
;  AUTHORS    Yutsudo,M.
;  TITLE      Direct Submission
;  JOURNAL    Submitted (17-JUN-1998) Masuo Yutsudo, Osaka University, Dept. of
;             Tumor Virol., Res. Inst. Microb. Dis.; 3-1 Yamadaoka, Suita, Osaka
;             565-0871, Japan (E-mail:yutsudo@biken.osaka-u.ac.jp,
;             Tel:81-6-879-8313, Fax:81-6-879-8315)
; FEATURES             Location/Qualifiers
;     source          1..2052
;                     /organism="Homo sapiens"
;                     /mol_type="mRNA"
;                     /db_xref="taxon:9606"
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;                     /gene="ASY"
;     CDS             67..1188
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;                     /protein_id="BAA83712.1"
;                     /db_xref="GI:5821140"
;                     /translation="MEDLDQSPLVSSDSPPRQPAFKYQFVREPEDEEEEEEEED
;             EDEDLEELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAP
;             ERQPCWDPSPVSSTVPAPSPLSAAAVSPSKLPQDDEPPARPPPPPASVSPQAEPVWT
;             PPAPAAPPSTPRAPKRRGSSGVVVDLLYWRDIKKTGVFGASLFLLLSLTVFSIV
;             SVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA
;             LGHVNCTIKBLRRLFLVDDLVDSLKFAVLMVVFTYVGALFNGLTLLLALISLFSVPV
;             IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"

; ORIGIN

; AB015639  Length: 2052  June 22, 2005 09:05  Type: N  Check: 3818  ..
ab015639

Alignment Scores:
Pred. No.:                 0                Length:              2052
Score:                  1825.80             Matches:              358
Percent Similarity:       96.25%            Conservative:           1
Best Local Similarity:    95.98%            Mismatches:             2
Query Match:              98.69%            Indels:                12
DB:                          1              Gaps:                   1

US-09-830-972-29-FUSED (1-361) x ab015639 (1-2052)

Qy     1 MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProProArgProGln  20
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    67 ATGGAAGACCTGGACCAGTCTCCTCTGGTCTCGTCCTCGGACAGCCCACCCGGCCGCCAG 126

Qy    21 ProAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGluGluGluGlu  40
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   127 CCCGGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAGGAAGAAGAGGAGGAG 186

Qy    41 GluGluGluAspGluAspGluAspLeuGluGluLeuGluValLeuGluArgLysProAla  60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   187 GAGGAGGAGGACGAGGACGAGGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAGCCCGCC 246

Qy    61 AlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp  80
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   247 GCCGGGCTGTCCGCGGCCCCAGTGCCCACGGCCCCGGCGGCCGGCGCCCCTGATGGAC 306

Qy    81 PheGlyAsnAspPheValProProAlaProArgGlyProLeuProAlaAlaProProVal 100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   307 TTCGGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCCCCGTC 366

Qy   101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrValProAlaPro 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   367 GCCCCGGAGCGGCAGCCGTGTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCGGCCCCA 426

Qy   121 SerProLeuSerAlaAlaAlaValSerProSerLysLeuProGlnAspAspGluProPro 140
           |||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db   427 TCCCCGCTGTCTGCCGCCGCAGTCTCGCCCTCCAAGCTCCCTCAGGACGACGAGCCTCCG 486

Qy   141 AlaArgProProProProAlaSerValSerProGlnAlaGluProValTrpThr 160
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gene    /organism="Homo sapiens"
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CDS     67..188
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        /db_xref="GI:5821140"
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        BRQPCWDPSPVSSTVAPSPLSAAAVSPSKLPQDDEPPARPPPPPASVSPQAEPVWT
        PPAPAPAPPSTPAAPKRQRGSSGSVVDLLWRDIKTGVVFGASLFLLSLTVFSIV
        SVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISELVQKYSNSA
        LGHVNCTIKELRRLFLVDDLVDSLKFAVLMVFTYVGALFNGLTLLILALISLFSVPV
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ORIGIN
; AB015639   Length: 2052   June 22, 2005 09:05   Type: N   Check: 3818  ..
ab015639

Alignment Scores:
Pred. No.:                              Length:              2052
Score:                      0           Matches:             58
Percent Similarity:    29.05%           Conservative:        12
Best Local Similarity: 24.07%           Mismatches:          78
Query Match:            6.04%           Indels:              93
                        1               Gaps:                12
DB:

Score: 111.70

US-09-830-972-29-FUSED (1-361) x ab015639 (1-2052)

Qy      6 GlnSerProLeuValSer-----------SerAspSerProProArg  18
          |||:::|||||   |||||
Db    673 CAAACACCACTCCAGTCTTCTAATGTCTCCCAGTACAGAGGTCAACACCACTGAGC  614

Qy     19 ProGln-------------  20
          |||:::
Db    613 CCGAGGAGCCCCTGCCTGGGCCGCCGCCGGTGCCGGGGGCGGGGGGGAGCCCGGG  554

Qy     21 ---ProAlaPheLysTyrGlnPheValArgGluProGlu  32
             ||||||||||||||
Db    553 CTGGCCGGGGTCCACACGGGGCTGCCTGGGGGCTCA------------CGTGGCCGGGG  506

Qy     33 AspGluGluGluGluGluGluGluGluGluGlyAspGluAspGluGluLeu  52
          :::||||||||||
Db    505 GAGGAGGGGGAGGCCCGGGAGGCTCGTCGTCCTGGAGGGAGCTGGAGGCGGAGACTG  446

Qy     53 GluValLeuGluArgLysProAlaAlaGlyLeuSerAlaAlaProValProThrAlaPro  72
          ||:::
Db    445 ----------------CGGCAGCAGCAGCGCGGGGATGGCCGGGCCGGGCCACGG---TCGACGACACCG  401

Qy     73 AlaAlaGlyAlaProLeuMetAspPheGlyAsnAspPheValProProAlaProArgGly  92
          :::|||
Db    400 GGCTCGGGTCCC------------AACACGGCTCGCCGCTCCGGGGCGACGGGGG  359

Qy     93 ProLeuProAlaProValAlaPro-------------  102
          |||||
Db    358 GAGCGGCCGCCAGGGGTCCCGGGGCGGGCGGGGCGGGGGCGGGGCCGGGGGCGGGGCGGGG  299

Qy    103 -------GluArgGlnProSerTrpAspProSerProValSerSerThrValProAla  119
                 :::
Db    298 GGGGGCCGCCGGGCAGGGGCGGTGGGCACTGGGGCGACGCCCGGCGCGGGGGGCT  239

Qy    120 ProSerProLeuSerAlaAlaAlaValSerProSerLysLeuProGluAspGluPro  139
          |||||
Db    238 TCCTTCCA-------GCACCTCCAGCTCCTCCAGGTCTTCGTCCT---------CGTCCT  194

Qy    140 ProAlaArgProPro--------ProProProAlaSerValSer--  152
          |||||               :::
Db    193 CCTCTTCCTCCTCCGTCCTCTTCCTCCTCGTCCTCCGGCGTCCCTCACGAACTGGTACTTGA  134
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```
Db    487 GCCCGGCCGCCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCGGCCGTGTGGGACC  546
Qy    161 ProProAlaProAlaProAlaAlaProProSerThrSer-----  173
Db    547 CCGCCAGCCCCCGGCTCCCCGCGCCCTCCACCCGCCGCGCCCCGAGCGCGCAGGGGC  606

Qy    174 ------ValValAspLeuLeuTyrTyrArgAspIleLysThrGlyVal  188
Db    607 TCCTCGGGCTCAGTCGTTGTTGACCTCCTGTACTCTGGAGAGACATTAAGAGACTGGAGTG  666

Qy    189 ValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVal  208
Db    667 GTGTTTGGTGCCAGCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGAGCGTA  726

Qy    209 ThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPheArgIleTyrLysGly  228
Db    727 ACAGCCTACATTGCCTTGGCCCTTGCCTCTGTGACCATCAGCTTTAGGATATACAAGGGT  786

Qy    229 ValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSer  248
Db    787 GTGATCCAAGCTATCCAGAAATCAGATGAAGGGCCACCCATTCAGGGCCATATCTCGAATCT  846

Qy    249 GluValAlaIleSerGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisVal  268
Db    847 GAAGTTGCTATATCTGAGGAGTTGGTTCGAAGTACAGTAATTCTGCTCTTGGTCATGTG  906

Qy    269 AsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu  288
Db    907 AACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTG  966

Qy    289 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThr  308
Db    967 AAGTTTGCAGTTGTGATGTGGGTATTTACCTATGTTGGTGCCCTGTTTAATGGTCTGACA  1026

Qy    309 LeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGln  328
Db   1027 CTACTGATTTTGGCTCTCATTAGCCTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAG  1086

Qy    329 AlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLys  348
Db   1087 GCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAA  1146

Qy    349 IleGlnAlaLysIleProGlyLeuLysArgLysAlaGlu  361
Db   1147 ATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAA  1185
```

```
RESULT 2
ab015639/c
; TOIG of: ab015639   check: 3818   from: 1   to: 2052

LOCUS       AB015639     2052 bp    mRNA    linear   PRI 03-SEP-1999
DEFINITION  Homo sapiens ASY mRNA, complete cds.
ACCESSION   AB015639
VERSION     AB015639.1  GI:5821139
KEYWORDS    ASY.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2052)
  AUTHORS   Yutsudo,M.
  TITLE     Isolation of a cell death-inducing gene
  JOURNAL   Published Only in DataBase (1999)
REFERENCE   2  (bases 1 to 2052)
  AUTHORS   Yutsudo,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-1998) Masuo Yutsudo, Osaka University, Dept. of
            Tumor Virol., Res. Inst. Microb. Dis.; 3-1 Yamadaoka, Suita, Osaka
            565-0871, Japan (E-mail:yutsudo@biken.osaka-u.ac.jp,
            Tel:81-6-879-8313, Fax:81-6-879-8315)
FEATURES             Location/Qualifiers
     source          1..2052
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Qy   153  ---------------ProGlnAlaGluProValTrpThrProPro---  162
                        |||::::            |||  |||
Db   133  ACGCGGGCTGCCGCCGGGGGTGGGCTGTCCGAGGACGAGGAGGAGGACTGGTCCAGGT  74

Qy   163  --------AlaProAlaProAlaAlaProProSerThr  172
                  |||  |||||||||  :::
Db    73  CTTCCATGGCTGGAGGGTGGAGATGATGCTGCAGCTGCTGCCGCGCCGCGCCGGGGCCGCG  14

Qy   173  Ser  173
              |||
Db    13  TCT  11
```

Search completed: June 22, 2005, 09:17:30
Job time : 2 secs

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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:      June 22, 2005, 09:12:04 ; Search time 5 Seconds
                                        (without alignments)
                                        2.272 Million cell updates/sec

Title:        US-09-830-972-29-COPY
Perfect score: 5923
Sequence:    1 MEDLDQSPLVSSDSPPRRQ.........VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62
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             Ygapop 10.0 , Ygapext  0.5
             Fgapop  6.0 , Fgapext  7.0
             Delop   6.0 , Delext   7.0

Searched:    1 segs, 4822 residues

Total number of hits satisfying chosen parameters:       2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-OUT=ngs.res -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO_XLPXY -NEG_SCORES=0
-LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   abs70449.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                            SUMMARIES

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Result        Query
No.   Score Match Length DB ID        Description
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  1   5748  97.0  4822  1  abs70449        TOIG of: abs7044
c 2     96   1.6  4822  1  abs70449        TOIG of: abs7044

                           ALIGNMENTS

RESULT 1
abs70449
; TOIG of: abs70449  check: 9399  from: 1  to: 4822
; ID   ABS70449 standard; cDNA; 4822 BP.
; XX
; AC   ABS70449;
; XX
; DT   27-NOV-2002 (first entry)
; XX
; DE   Human bone remodelling gene #106.
; XX
; KW   Bone remodelling; osteoporosis; human; gene; ss.
; XX
; OS   Homo sapiens.
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; XX
; PN   US6426186-B1.
; XX
; PD   30-JUL-2002.
; XX
; PF   18-JAN-2000; 2000US-0048970.
; XX
; PR   18-JAN-2000; 2000US-0048970.
; XX
; PA   (INCY-) INCYTE GENOMICS INC.
; XX
; PI   Jones KA, Volkmuth W, Walker MG;
; XX
; DR   WPI; 2002-673014/72.
; XX
; PT   A combination of polynucleotides which are co-expressed with genes known
; PT   to be involved in bone remodeling and osteoporosis are useful in an array
; PT   for the diagnosis of bone remodeling and osteoporosis associated
; PT   disorders.
; XX
; PS   Claim 1; Col 283-288; 206pp; English.
; XX
; CC   The invention relates to a combination comprising a number of
; CC   substantially purified and isolated polynucleotides which are co-
; CC   expressed with genes known to be involved in bone remodeling and
; CC   osteoporosis. The invention is used to diagnose disorders associated with
; CC   bone remodelling or osteoporosis. ABS70344-ABS70512 represent human bone
; CC   remodelling genes of the invention
; XX
; SQ   Sequence 4822 BP; 1441 A; 1046 C; 1073 G; 1247 T; 0 U; 15 Other;
; ABS70449  Length: 4822  June 22, 2005 09:05  Type: N  Check: 9399 ..
abs70449

Alignment Scores:
Pred. No.:              0                    Length:          4822
Score:           5748.00                     Matches:         1155
Percent Similarity:   96.99%                 Conservative:       5
Best Local Similarity: 96.57%                Mismatches:        17
Query Match:          97.05%                 Indels:            19
DB:                                          Gaps:               3

US-09-830-972-29-COPY (1-1178) x abs70449 (1-4822)

Qy   1 MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProProArgProGln 20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 253 ATGGAAGACCTGGACCAGTCTCCTCTGGTCTCCTCGGACAGCCCACCCCGGCCGCCGCAG 312

Qy  21 ProAlaPheLysTyrGlnPheValArgGluProGluGluGluGluGlu 40
        ||||||||||||||||||||||||||||||||||||||||||  :::
Db 313 CCCGCGGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAGGAAGAGGAGGANGAT 372

Qy  41 GluGluGluAspGluAspGluAspLeuGluLeuGluValLeuGluArgLysProAla 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 373 GAAGAGGAGGAGGACGAAGACCTGGAGCTGGAGGTGCTGGAGAGGAAGCCCGCC 432

Qy  61 AlaGlyLeuSerAlaAlaProThrAlaProAlaAlaGlyAlaProLeuMetAsp 80
        |||||||||||||||||||||||||||||||||||||||||||||||  ||||
Db 433 GCCGGGCTGTCCGCGGCCGCCCAGTGCCCACCGCCGGCGCCCNTAATGGAC 492

Qy  81 PheGlyAsnAspPheValProAlaProArgGlyProLeuProAlaAlaProProVal 100
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 493 TTCGGAAATGACTTCGTGCCCGCGGGACCCCTGCCGGCCGCTCCCCCGTC 552

Qy 101 AlaProGluArgGlnProSerProSerTrpAspProSerSerSerThrValProAlaPro 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 553 GCCCCGGAGCGGCAGCCGCCGTCTTGGGACCCGAGCCCGGTCGTCGCCGCCCGCCA 612

Qy 121 SerProLeuSerAlaAlaAlaValSerProSerLysLeuProGluAspAspProPro 140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 613 TCCCCGCTGTCCGCCGCCGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGAGCCTCCG 672

Qy 141 AlaArgProProProProAlaSerValSerProGlnAlaProValProValTrpThr 160
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Right column (Db / Qy alignment blocks):

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Db        GAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAACCCTTTACTTG   1812
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1753 Db

 506 Qy   alAlaAlaGlnAspSerGluThrAspTyrArgValThrThrAspAsnLeuThrLysValThrG    526
1813 Db   TAGCACCAGACAGATTCTGAGACAGATATGTCACAACAGATAATTTAACAAAGGTGACTG   1872

 526 Qy   luGluValValAlaAlaAsnMetProGluGlyLeuThrProAspLeuValGlnGluAlaCysG    546
1873 Db   AGGAAGTCGTTGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAGGAAGCATGTG   1932

 546 Qy   luSerGluLeuLeuLysGluGlnProGlyAsnThrIleSerIleAlaTyrGluThrLysAspLeuV    566
1933 Db   AAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGGACAAAAATGGACTTGG   1992

 566 Qy   alGlnThrSerGluValMetGluGlnProAlaAlaGlnLeuCysProSerP    586
1993 Db   TTCAAACATCAGAAGTTATGCAAGAGCACTCTATCCTGCAGCACAGCTTTGCCCATCAT   2052

 586 Qy   heGluGluSerGluAlaThrProSerProValLeuProAspIleValMetGluAlaProL    606
2053 Db   TTGAAGAGTCAGAAGCTACTCCTTCACCCAGTTGCCTGACATTGTTATGGAAGCACCAT   2112

 606 Qy   euAsnSerAlaValProSerAlaGlyAlaSerValIleGlnProSerProLeuG    626
2113 Db   TGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCATCACCATTAG   2172

 626 Qy   luAlaSerSerValAsnTyrGluSerIleLysHisGluProGluAsnProProTyrG    646
2173 Db   AAGCTTCTTCAGTTAATTATGAAAGCATAAAGCATGAGCCTGAAAACCCCACCATATG   2232

 646 Qy   luGluAlaMetSerValSerLeu--LysValSerGlyLyIleLysGluIleLysGluP    665
2233 Db   AAGAGGCCATGAGTGTATCACTAAAAAGTATCAGGAATAAAGGAGAAATTAAAGAGC   2292

 665 Qy   roGlyAsnIleAsnAlaAlaLeuGlnGluThrGluAlaProTyrIleSerIleAlaCysA    685
2293 Db   CTGAAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATCTATTGCATGTG   2352

 685 Qy   spLeuIleLeuLysGlyThrLysLeuSerAlaGluProAlaProAspPheSerAspTyrSerG    705
2353 Db   ATTTAATTAAAGAAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTCTCTGATTATTCAG   2412

 705 Qy   luMetAlaLysAlaGluGlnProAspHisSerGluLeuValGluLysAspSerSerP    725
2413 Db   AAATGGCAAAAGTTGAACAGCCCAGTGCCTAGCATCTCGAGCTAGTTGAAGATTCCTCAC   2472

 725 Qy   roAspSerGluProValAspLeuPheSerArgAspAspSerIleProAspValProGlnLysG    745
2473 Db   CTGATTCTGAACCAGTTGACTTATTTAGTAGAGATGATTCAATACCTGACGTTCCACAAAAC   2532

 745 Qy   lnAspGluThrValMetLeuValLysGluSerLeuThrSerPheGluMetI    765
2533 Db   AAGATGAAACTGTGATGCTTGTGAAAGAAAGCTCCACTGAGACTTCATTTGAATGA   2592

 765 Qy   leGluSerPheLysLeuSerLeuGluSerLeuThrSerPheGluProGluTyrL    785
2593 Db   TGGAAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCGTTACCTGATGAAGTTT   2652

 785 Qy   euGluSerLysLysSerGluLysIleProLeuGlnMetGluGluLeuSerThrAlaValS    805
2653 Db   TGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCGTTACCTGATGAAGTTT   2712

 805 Qy   erThrLeuSerLysLysSerAspAspArgSerLysLysIleGluArgGluThrGluAlaValT    825
2713 Db   CAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTCAGTACTGCAGTTT   2772

 825 Qy   yrSerArgAsnAspAspLeuPheIleSerSerLysValAlaGlnIleLeuArgGluThrGluPheS    845
2773 Db   ATTCAAATGATGACTTTATTTATTTCAAGGAAGCACAAGATAAGAACTGAAAACGTTTT   2832

 845 Qy   erAspSerSerProIleGluIleLeuAspGluProThrLeuIleSerSerLysThrAr    865
2833 Db   CAGATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACAATTGATCAGTTCAAAAACTG   2892
```

Left column (Qy / Db alignment blocks):

```
 673 Db   GCCCGGCCTCCCCGTCCTCCCCGGCCAGCCGAGCCCAGGCAGAGCCCGTGTGGANC   732
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 161 Qy   ProProAlaProAlaProAlaProSerThrProAlaAlaProLysArgArgGly   180
 733 Db   CCGCCAGCCCCGGCTNCCGCCGGCCCCCCCCCCGGCCGCGCCAAGCCGCAGGGGC   792

 181 Qy   SerSerGlyAla------------------ValVal   186
 793 Db   TCCTCCGGCTCAGTGCATGGATGAGACCCTTTTGCTCTCCTGCTGCATCTGAGCCTGTGATA   852

 187 Qy   **********LysIleMetAspLeuLysGluGlnProGlyAsnThrIleSerAlaGly   206
 853 Db   CGCTCCTCTGCAGAAAATATGGACTTGAAGGAGCAGCCAGTAACACTATTCCGGCTGGT   912

 207 Qy   GlnGluAspPheProSerValLeuLeuGluThrAlaAlaSer***ProSerLeuSerPro   226
 913 Db   CAAGAGGAATTCCCATCTGTCCTGCTGCTTCCTCTCTCCTTCTGTCTCCT   972

 227 Qy   LeuSerAlaAlaSerPheLysGluHisGluTyrLeuGlyAsnLeuSerThrValLeuPro   246
 973 Db   CTCTCAGCCGCGCTTCTTCAGAACAATGAATACCTTGGTAATTTGTCAACAGTATTACCC   1032

 247 Qy   ThrGluGlyThrLeuThrLeuGlnGluAsnValSerGluAlaSerLysGluValSerGluLysAla   266
1033 Db   ACTGAAGGAACACTTCAGAGAAAATGTCAGTGAAGCTTCTAAAGACGTCTCAGAAGAAGGCA   1092

 267 Qy   LysThrLeuLeuIleAspArgAspPheLeuThrGluSerGluThrGluThrTyrSerGluMet   286
1093 Db   AAAACTCTACTACTCATAGATAGAGATTTAACAGAGAGTTTTCAGAATACTCAGAAATG   1152

 287 Qy   GlySerSerPheSerValSerProLysSerAlaGluValAlaIleGluValAlaAsnProArg   306
1153 Db   GGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCAAATCCTAGG   1212

 307 Qy   GluGluIleIleValLysAsnLysAspGluGlyLeuLysLeuAsnValSerArgAsnAsnIleLeu   326
1213 Db   GAAGAGAATAATGCTGAAAAATAAAGATGAAGAGAAGAAGTTAGTTAGTAATAACATCCTT   1272

 327 Qy   His****GlnIleGluLeuProThrAlaLeuThrLysValGluValLysGluValAspGluValVal   346
1273 Db   CATAATCAACAGAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGATGAAGTTGTG   1332

 347 Qy   SerSerGluLysAlaLysAlaAspSerPheAsnGlyLysArgValLysArgValAlaValGluAlaProMet   366
1333 Db   TCTTCAGAAAAAGCAAAAGCAGATTTTAATGAAAAGAGAGTTGCAGTGGAAGCTCCTATG   1392

 367 Qy   ArgGluGluTyrArgIleAspSerPheLysProPheLysTrpGluValValLysValAspSerLys   386
1393 Db   AGGGAAGAATATAGGATTGACTTCAAACCATTTAGCCAGTATGGGAAGTGAAAGATAGTAAG   1452

 387 Qy   GluAspSerAsnMetLeuAlaAlaGlyTyrGlyTyrIleGluLysAsnGluLysLysVal   406
1453 Db   GAAGATAGTAGTATGTTGGCTGCTGGATATGGTTATATTGAGAAGAATGAGAAAAGTAAAGTG   1512

 407 Qy   AspLysLysCysPheAlaProSerLeuGlnThrAsnHisGluLeuGluAspSerGlyAla   426
1513 Db   GATAAAAAATGTTTGCAAGATCCTTCTTTGCAGACGAATATAGCAACAAACATTTTT   1572

 427 Qy   SerAsnAspThrSerAspPheProSerLeuGluGlnThrAsnHisGluLeuGluAspSerGlyAla   446
1573 Db   AGTAATGATGATACTTCTTTTCCCCAGTACGGAAGGTATAAAGGATCGTTCAGGAGCA   1632

 447 Qy   TyrIlePheCysLysAlaProPheAsnProAlaAlaThrGluSerIleAlaThrAsnIlePhe   466
1633 Db   TATATCACCATGTGCTCCCTTTAACCCAGCAGCAATTGCAACAAACATTTTT   1692

 467 Qy   ProLeuLeuGluAspProThrSerGluAsn***ThrAspPheGlu--LysLysIleGluGluLy   486
1693 Db   CCTTTTGTTAGGAGATCCCACTTCAGAAATAGACCGATGAAAAAAAATAGAAGAAAA   1752

 486 Qy   sLysAlaGlnIleValThrGluLysThrGlyAsnThrSerThrAsnProPhe--PheV   506
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```
; DT   27-NOV-2002 (first entry)
; XX
; DE   Human bone remodelling gene #106.
; XX
; KW   Bone remodelling; osteoporosis; human; gene; ss.
; XX
; OS   Homo sapiens.
; XX
; PN   US6426186-B1.
; XX
; PD   30-JUL-2002.
; XX
; PF   18-JAN-2000; 2000US-00484970.
; XX
; PR   18-JAN-2000; 2000US-00484970.
; XX
; PA   (INCY-) INCYTE GENOMICS INC.
; XX
; PI   Jones KA, Volkmuth W, Walker MG;
; XX
; DR   WPI; 2002-673014/72.
; XX
; PT   A combination of polynucleotides which are co-expressed with genes known
; PT   to be involved in bone remodeling and osteoporosis are useful in an array
; PT   for the diagnosis of bone remodeling and osteoporosis associated
; XX   disorders.
; XX
; PS   Claim 1; Col 283-288; 206pp; English.
; XX
; CC   The invention relates to a combination comprising a number of
; CC   substantially purified and isolated polynucleotides which are co-
; CC   expressed with genes known to be involved in bone remodelling and
; CC   osteoporosis. The invention is used to diagnose disorders associated with
; CC   bone remodeling or osteoporosis. ABS70344-ABS70512 represent human bone
; CC   remodelling genes of the invention
; XX
; SQ   Sequence 4822 BP; 1441 A; 1046 C; 1073 G; 1247 T; 0 U; 15 Other;
;
; ABS70449  Length: 4822   June 22, 2005 09:05   Type: N   Check: 9399  ..
abs70449

Alignment Scores:
Pred. No.:                0              Length:          4822
Score:                    96.00         Matches:         42
Percent Similarity:       31.93%        Conservative:    11
Best Local Similarity:    25.30%        Mismatches:      61
Query Match:              1.62%         Indels:          52
DB:                       1             Gaps:            7

US-09-830-972-29-COPY (1-1178) x abs70449 (1-4822)

Qy   29 ArgGluProGluAspGluGluGluGluGluGluGluGluAspGluGluAspGluAsp 48
Db  703 CGCTGGCCGCGGGGAGGAGGGGGAGGCCGGGCCTCGTCGTCCTCAGGGAGCTTGG 644
Qy   49 LeuGluGluLeuGluValLeuGluLeuArgLysProAlaAlaGlyLeuSerAlaAlaAlaProVal 68
Db  643 AGGGCGGAGACTG----------CGGCAGCAGACAGCGGGATGGCGCGGGCACGG--- 599
Qy   69 ProThrAlaProAlaAlaGlyTyrProLeuMetAspPheGlyAsnAspPheValProPro 88
Db  598 TCGACGACACCGGCTCGGGTCC------------AAGACGGCTGCCGCCTCCG 557
Qy   89 AlaProAlaArgGlyProLeuProAlaAlaProValAlaPro---------------- 102
Db  556 GGGGCGACGGGGGACGGGGGAGCGGGGGTCCCCGGGCGCCGCGGCGGAGTCATTC 497
Qy  103 ------------GluArgGlnProSerTrpAspProSerProValSerSer 115
Db  496 CGAAGTCCATTANNGGCGCGCGCGGCACTGGGCGCGGGCACCAGCC 437
Qy  116 ThrValProAlaProSerProLeuSerAlaAlaAlaAlaValSerProLysLysLeuProGlu 135
```

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Qy  865 spSerPheSerLysTyrLeuAlaAlaArgGluTyrThrAspLeuGluValSerHisLysSerGluI 885
Db 2893 ATTCATTTTCTAAATTAGCACGGGAATATACTGACCTAGAAGTATCCCACAAAAGTGAAA 2952
Qy  885 leAlaAlaAsnAlaProAspGlyAlaGlySerLeuProCysThrGluLeuProHisAspLeuS 905
Db 2953 TTGCTAATGCCCCGACTGGAGCTGGGTCATTGCCTTGCACAGAGAATTGCCCCATGACCTTT 3012
Qy  905 erLeuLysAsnIleGlnProLysValGlyGluLysIleSerPheSerAspAspPheSerLeuL 925
Db 3013 CTTTGAGAGACATACACCCAAAGTTGAAGAGAAAATCAGTTTCTCAGATGACTTTTCTA 3072
Qy  925 ysAsnGlySerAlaThrSerLysLysValLeuLeuLeuProProAspValSerAlaLeuGlyH 945
Db 3073 AAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTTTCTGCTTTGGCC-- 3131
Qy  945 isThrGlnIleAlaGluIleGluSerIleValLysProLysValLeuGluGluLysGluGluL 965
Db 3132 --ACTCAAGCAGAGAGACATAGTTAAACCCAAAGTTCTTGTGAAAGAAGCTGAGA 3189
Qy  965 ysLysLeuProSerAspThrGluLysAspArgSerProSerAlaIlePheSerAlaAlaA 985
Db 3190 AAAAACTTCCTTCCGATACAGAAAAGAAGGACAGATCACCATCTGCTATATTTTCAGCAG 3249
Qy  985 spLeu-GlyLysThrSerValValAspLeuLeuLeuTyrThrArgAspIleLysLysLysThrGly 1004
Db 3250 AGCTGAGCTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGA 3309
Qy 1005 ValValPheGlyAlaSerLeuPheLeuLeuLeuLeuSerLeuLeuPheSerIleValSer 1024
Db 3310 GTGGGTGTTTGGTGCCAGCTATTCCTGCTTTCATTGACGTATTCAGCATTGTGAGC 3369
Qy 1025 ValThrAlaTyrIleAlaLeuAlaLeuAsnLeuSerValThrIleSerPheArgIleTyrLys 1044
Db 3370 GTAACAGCTACATTGCCTTGGCCTCTGTCTCTGTGACCATCAGCTTAGGATATACAG 3429
Qy 1045 GlyValIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGlu 1064
Db 3430 GGTGTGATCCAAGCTATCCAGAAATCAGATGAGAAGGCCACCCATTCAGGGCATATCTGAA 3489
Qy 1065 SerGluValAlaIleIleSerGluGluLeuValGlnLysTyrArgSerAsnSerAlaLeuGlyHis 1084
Db 3490 TCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCAT 3549
Qy 1085 ValAsnCysThrIleLysValGluLysArgLeuPheLeuValAspAspPheLeuValAspSer 1104
Db 3550 GTGAACTGCACGATAAAGGAACTCAGGCGCCCTCTTCTTACTTTAGTTGATTCT 3609
Qy 1105 LeuLysPheAlaAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeu 1124
Db 3610 CTGAAGTTTGCAGTGTTGAGTGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTG 3669
Qy 1125 ThrLeuLeuIleLeuAlaLeuIleLeuSerLeuPheSerValProValIleTyrGluArgHis 1144
Db 3670 ACACTACTGATTTTGGCTCTCATTTCACTGTTCCTGTTATTTATGAACGGCAT 3729
Qy 1145 GlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValAlaAspAlaMetAla 1164
Db 3730 CAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTATGCTATGCT 3789
Qy 1165 LysIleGlnAlaLysIleProGlyLeuGluLysArgLysAlaGlu 1178
Db 3790 AAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGAA 3831

RESULT 2
abs70449/c
; TOIG of: abs70449  check: 9399  from: 1  to: 4822
; XX
; ID   ABS70449  standard; cDNA; 4822 BP.
; XX
; AC   ABS70449;
; XX
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Db    436  CGGCGGCGGGCTTCCTCT-------------------------------------------  419

Qy    136  AspAspGluProProAlaArgProProProProProAlaSerValSerProGlnAla  155
                |||   ||||||||||||  |||           :::  |||   |||:::
Db    418  ----------------------CCAGCACCTCCAGTCCTCCAGGTCTTCGTCCTCGT----  383

Qy    156  GluProValTrpThrProProAlaAlaProAlaAlaProProSerThrProAlaAla  175
                |||||    |||   |||||  |||         |||         |||
Db    382  -------------------CCTCCCTTCATCNTCCTCTTCCTCCT---CGTCCTCGGGCT  341

Qy    176  ProLysArgArgGlySer  181
                |||   |||   |||:::
Db    340  CCCTCACGAACTGGTACT  323


Search completed: June 22, 2005, 09:12:28
Job time : 23 secs
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